

SEQUENCE LISTING

<110> Kline, Kimberly
Sanders, Bob G.
Yu, Weiping

<120> Mutant p53 Proteins And Uses Thereof

<130> D6454CIP

<140>
<141> 2003-10-29
<150> US 10/444,287
<151> 2003-05-23

<160> 9

<210> 1
<211> 1161
<212> DNA
<213> *Homo sapiens*

<220>

<221> mat_peptide
<223> cDNA sequence of mutant p53 (Δ 126-132)

<400> 1

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aacattttca	gacctatgga	aactacttcc	tgaaaacaac	gttctgtccc	100
ccttgccgtc	ccaagcaatg	gatgatttga	tgctgtcccc	ggacgatatt	150
gaacaatggt	tactgaaga	cccaggtcca	gatgaagctc	ccagaatgcc	200
agaggctgct	ccccccgtgg	cccctgcacc	agcagctcct	acaccggcgg	250
cccctgcacc	agccccctcc	tggcccctgt	catcttctgt	cccttcccag	300
aaaacctacc	agggcagcta	cggtttccgt	ctgggcttct	tgcatctctg	350
gacagccaag	tctgtgactt	gcacgatgtt	ttgccaaactg	gccaagacct	400
gccctgtgca	gctgtggggt	gattccacac	ccccgcccgg	caccgcgctc	450
cgcgccatgg	ccatctacaa	gcagtcacag	cacatgacgg	aggttgtgag	500
gcgctgcccc	caccatgagc	gctgctcaga	tagcgatggt	ctggccccctc	550
ctcagcatct	tatccgagtg	gaaggaaatt	tgctgttgga	gtatttgga	600
gacagaaaca	cttttcgaca	tagtgtggtg	gtgccctatg	agccgcctga	650
ggttggctct	gactgtacca	ccatccacta	caactacatg	tgtaacagtt	700
cctgcatggg	cggcatgaac	cggaggccca	tcctcaccat	catcacactg	750
gaagactcca	gtggtaatct	actgggacgg	aacagctttg	agggtgcatgt	800
ttgtgcctgt	cctgggagag	accggcgcac	agaggaagag	aatctccgca	850
agaaagggga	gcctcaccac	gagctgcccc	caggagcac	taagcgagca	900
ctgcccaaca	acaccagctc	ctctccccag	ccaaagaaga	aaccactgga	950
tggagaatat	ttcacccttc	agatccgtgg	gcgtgagcgc	ttcgagatgt	1000
tccgagagct	gaatgaggcc	ttggaactca	aggatgccca	ggctgggaag	1050
gagccagggg	ggagcagggc	tactccagc	cacctgaagt	ccaaaagggg	1100
tcagtctacc	tcccgccata	aaaaactcat	gttcaagaca	gaagggcctg	1150
actcagactg	a				1161

<210> 2
 <211> 386
 <212> PRT
 <213> *Homo sapiens*

<220>

<221> PEPTIDE
 <223> mutant p53 (Δ 126-132)

<400> 2

Met	Glu	Glu	Pro	Gln	Ser	Asp	Pro	Ser	Val	Glu	Pro	Pro	Leu	Ser	5	10	15
Gln	Glu	Thr	Phe	Ser	Asp	Leu	Trp	Lys	Leu	Leu	Pro	Glu	Asn	Asn	20	25	30
Val	Leu	Ser	Pro	Leu	Pro	Ser	Gln	Ala	Met	Asp	Asp	Leu	Met	Leu	35	40	45
Ser	Pro	Asp	Asp	Ile	Glu	Gln	Trp	Phe	Thr	Glu	Asp	Pro	Gly	Pro	50	55	60
Asp	Glu	Ala	Pro	Arg	Met	Pro	Glu	Ala	Ala	Pro	Pro	Val	Ala	Pro	65	70	75
Ala	Pro	Ala	Ala	Pro	Thr	Pro	Ala	Ala	Pro	Ala	Pro	Ala	Pro	Ser	80	85	90
Trp	Pro	Leu	Ser	Ser	Ser	Val	Pro	Ser	Gln	Lys	Thr	Tyr	Gln	Gly	95	100	105
Ser	Tyr	Gly	Phe	Arg	Leu	Gly	Phe	Leu	His	Ser	Gly	Thr	Ala	Lys	110	115	120
Ser	Val	Thr	Cys	Thr	Met	Phe	Cys	Gln	Leu	Ala	Lys	Thr	Cys	Pro	125	130	135
Val	Gln	Leu	Trp	Val	Asp	Ser	Thr	Pro	Pro	Pro	Gly	Thr	Arg	Val	140	145	150
Arg	Ala	Met	Ala	Ile	Tyr	Lys	Gln	Ser	Gln	His	Met	Thr	Glu	Val	155	160	165
Val	Arg	Arg	Cys	Pro	His	His	Glu	Arg	Cys	Ser	Asp	Ser	Asp	Gly	170	175	180
Leu	Ala	Pro	Pro	Gln	His	Leu	Ile	Arg	Val	Glu	Gly	Asn	Leu	Arg	185	190	195
Val	Glu	Tyr	Leu	Asp	Asp	Arg	Asn	Thr	Phe	Arg	His	Ser	Val	Val	200	205	210
Val	Pro	Tyr	Glu	Pro	Pro	Glu	Val	Gly	Ser	Asp	Cys	Thr	Thr	Ile	215	220	225
His	Tyr	Asn	Tyr	Met	Cys	Asn	Ser	Ser	Cys	Met	Gly	Gly	Met	Asn	230	235	240
Arg	Arg	Pro	Ile	Leu	Thr	Ile	Ile	Thr	Leu	Glu	Asp	Ser	Ser	Gly	245	250	255
Asn	Leu	Leu	Gly	Arg	Asn	Ser	Phe	Glu	Val	His	Val	Cys	Ala	Cys	260	265	270
Pro	Gly	Arg	Asp	Arg	Arg	Thr	Glu	Glu	Glu	Asn	Leu	Arg	Lys	Lys	275	280	285
Gly	Glu	Pro	His	His	Glu	Leu	Pro	Pro	Gly	Ser	Thr	Lys	Arg	Ala	290	295	300
Leu	Pro	Asn	Asn	Thr	Ser	Ser	Ser	Pro	Gln	Pro	Lys	Lys	Lys	Pro			

Leu	Asp	Gly	Glu	Tyr	Phe	Thr	Leu	Gln	Ile	Arg	Gly	Arg	Glu	Arg	305	310	315
															320	325	330
Phe	Glu	Met	Phe	Arg	Glu	Leu	Asn	Glu	Ala	Leu	Glu	Leu	Lys	Asp	335	340	345
Ala	Gln	Ala	Gly	Lys	Glu	Pro	Gly	Gly	Ser	Arg	Ala	His	Ser	Ser	350	355	360
His	Leu	Lys	Ser	Lys	Lys	Gly	Gln	Ser	Thr	Ser	Arg	His	Lys	Lys	365	370	375
Leu	Met	Phe	Lys	Thr	Glu	Gly	Pro	Asp	Ser	Asp					380	385	

<210> 3
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>

<221> primer_bind
 <223> sense primer for p53

<400> 3
 atggaggagc cgagtcaga t 21

<210> 4
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>

<221> primer_bind
 <223> anti-sense primer for p53

<400> 4
 tcagtctgag tcaggccctt c 21

<210> 5
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>

<221> primer_bind
 <223> sense primer for p53, encoding an EcoRI restriction
 enzyme cutting site, starting codon, HA residue,
 and p53 sequence from 4-21 nucleotide bases

<400> 5
 cgcgattca tgtatgatgt tcctgattat gctagcctcg aggagccgca 50

gtcagatcct

60

<210> 6
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<221> primer_bind
<223> anti-sense primer for p53, containing a BamHI
restriction enzyme cutting site and stop codon

<400> 6
cgcgcatcct cagtctgagt caggcccttc 30

<210> 7
<211> 393
<212> PRT
<213> *Homo sapiens*

<220>

<221> PEPTIDE
<223> wild-type p53

<400> 7
Met Glu Glu Pro Gln Ser Asp Pro Ser Val Glu Pro Pro Leu Ser
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Gln Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro Glu Asn Asn
20 25 30
Val Leu Ser Pro Leu Pro Ser Gln Ala Met Asp Asp Leu Met Leu
35 40 45
Ser Pro Asp Asp Ile Glu Gln Trp Phe Thr Glu Asp Pro Gly Pro
50 55 60
Asp Glu Ala Pro Arg Met Pro Glu Ala Ala Pro Pro Val Ala Pro
65 70 75
Ala Pro Ala Ala Pro Thr Pro Ala Ala Pro Ala Pro Ala Pro Ser
80 85 90
Trp Pro Leu Ser Ser Ser Val Pro Ser Gln Lys Thr Tyr Gln Gly
95 100 105
Ser Tyr Gly Phe Arg Leu Gly Phe Leu Ser Gly Thr Ala Lys
110 115 120
Ser Val Thr Cys Thr Tyr Ser Pro Ala Leu Asn Lys Met Phe Cys
125 130 135
Gln Leu Ala Lys Thr Cys Pro Val Gln Leu Trp Val Asp Ser Thr
140 145 150
Pro Pro Pro Gly Thr Arg Val Arg Ala Met Ala Ile Tyr Lys Gln
155 160 165
Ser Gln His Met Thr Glu Val Val Arg Arg Cys Pro His His Glu
170 175 180
Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln His Leu Ile

SEQ 4

				185					190					195
Arg	Val	Glu	Gly	Asn	Leu	Arg	Val	Glu	Tyr	Leu	Asp	Asp	Arg	Asn
				200					205					210
Thr	Phe	Arg	His	Ser	Val	Val	Val	Pro	Tyr	Glu	Pro	Pro	Glu	Val
				215					220					225
Gly	Ser	Asp	Cys	Thr	Thr	Ile	His	Tyr	Asn	Tyr	Met	Cys	Asn	Ser
				230					235					240
Ser	Cys	Met	Gly	Gly	Met	Asn	Arg	Arg	Pro	Ile	Leu	Thr	Ile	Ile
				245					250					255
Thr	Leu	Glu	Asp	Ser	Ser	Gly	Asn	Leu	Leu	Gly	Arg	Asn	Ser	Phe
				260					265					270
Glu	Val	Arg	Val	Cys	Ala	Cys	Pro	Gly	Arg	Asp	Arg	Arg	Thr	Glu
				275					280					285
Glu	Glu	Asn	Leu	Arg	Lys	Lys	Gly	Glu	Pro	His	His	Glu	Leu	Pro
				290					295					300
Pro	Gly	Ser	Thr	Lys	Arg	Ala	Leu	Pro	Asn	Asn	Thr	Ser	Ser	Ser
				305					310					315
Pro	Gln	Pro	Lys	Lys	Lys	Pro	Leu	Asp	Gly	Glu	Tyr	Phe	Thr	Leu
				320					325					330
Gln	Ile	Arg	Gly	Arg	Glu	Arg	Phe	Glu	Met	Phe	Arg	Glu	Leu	Asn
				335					340					345
Glu	Ala	Leu	Glu	Leu	Lys	Asp	Ala	Gln	Ala	Gly	Lys	Glu	Pro	Gly
				350					355					360
Gly	Ser	Arg	Ala	His	Ser	Ser	His	Leu	Lys	Ser	Lys	Lys	Gly	Gln
				365					370					375
Ser	Thr	Ser	Arg	His	Lys	Lys	Leu	Met	Phe	Lys	Thr	Glu	Gly	Pro
				380					385					390
Asp	Ser	Asp												
				393										

<210> 8
 <211> 359
 <212> PRT
 <213> *Homo sapiens*

<220>

<221> PEPTIDE
 <223> p53 double mutant (Δ 126-132+ Δ 367-393)

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Gln	Glu	Thr	Phe	Ser	Asp	Leu	Trp	Lys	Leu	Leu	Pro	Glu	Asn	Asn
				20					25					30
Val	Leu	Ser	Pro	Leu	Pro	Ser	Gln	Ala	Met	Asp	Asp	Leu	Met	Leu
				35					40					45
Ser	Pro	Asp	Asp	Ile	Glu	Gln	Trp	Phe	Thr	Glu	Asp	Pro	Gly	Pro
				50					55					60
Asp	Glu	Ala	Pro	Arg	Met	Pro	Glu	Ala	Ala	Pro	Pro	Val	Ala	Pro
				65					70					75
Ala	Pro	Ala	Ala	Pro	Thr	Pro	Ala	Ala	Pro	Ala	Pro	Ala	Pro	Ser

Trp	Pro	Leu	Ser	80	Ser	Ser	Val	Pro	Ser	85	Gln	Lys	Thr	Tyr	Gln	90	Gly
				95	Arg	Leu	Gly	Phe	Leu	100	Ser	Gly	Thr	Ala	Lys	105	
Ser	Tyr	Gly	Phe	110	Thr	Met	Phe	Cys	Gln	115	Leu	Ala	Lys	Thr	Cys	120	Pro
Ser	Val	Thr	Cys	125	Val	Asp	Ser	Thr	Pro	130	Pro	Pro	Gly	Thr	Arg	135	Val
Val	Gln	Leu	Trp	140	Ile	Tyr	Lys	Gln	Ser	145	Gln	His	Met	Thr	Glu	150	Val
Arg	Ala	Met	Ala	155	Pro	His	His	Glu	Arg	160	Cys	Ser	Asp	Ser	Asp	165	Gly
Val	Arg	Arg	Cys	170	Gln	His	Leu	Ile	Arg	175	Val	Glu	Gly	Asn	Leu	180	Arg
Leu	Ala	Pro	Pro	185	Asp	Asp	Arg	Asn	Thr	190	Phe	Arg	His	Ser	Val	195	Val
Val	Glu	Tyr	Leu	200	Pro	Pro	Glu	Val	Gly	205	Ser	Asp	Cys	Thr	Thr	210	Ile
Val	Pro	Tyr	Glu	215	Met	Cys	Asn	Ser	Ser	220	Cys	Met	Gly	Gly	Met	225	Asn
His	Tyr	Asn	Tyr	230	Leu	Thr	Ile	Ile	Thr	235	Leu	Glu	Asp	Ser	Ser	240	Gly
Arg	Arg	Pro	Ile	245	Arg	Asn	Ser	Phe	Glu	250	Val	Arg	Val	Cys	Ala	255	Cys
Asn	Leu	Leu	Gly	260	Arg	Arg	Thr	Glu	Glu	265	Glu	Asn	Leu	Arg	Lys	270	Lys
Pro	Gly	Arg	Asp	275	His	Glu	Leu	Pro	Pro	280	Gly	Ser	Thr	Lys	Arg	285	Ala
Gly	Glu	Pro	His	290	Thr	Ser	Ser	Ser	Pro	295	Gln	Pro	Lys	Lys	Lys	300	Pro
Leu	Pro	Asn	Asn	305	Tyr	Phe	Thr	Leu	Gln	310	Ile	Arg	Gly	Arg	Glu	315	Arg
Leu	Asp	Gly	Glu	320	Arg	Glu	Leu	Asn	Glu	325	Ala	Leu	Glu	Leu	Lys	330	Asp
Phe	Glu	Met	Phe	335	Lys	Glu	Pro	Gly	Gly	340	Ser	Arg	Ala	His	Ser	345	
Ala	Gln	Ala	Gly	350						355						359	

<210> 9
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>

<221> primer_bind
 <223> anti-sense primer for TM p53 and p53 double mutant

<400> 9
 gcgtctagat caggagtgag ccctgctccc 30